

THEORY



#22

61 Met Val Asn Ala Trp Thr Pro Ser Ser Asn Asp Asp Asn Pro Trp Ile

RAW SEQUENCE LISTING

DATE: 04/17/2003

PATENT APPLICATION: US/09/582,340C

TIME: 18:18:17

Input Set : A:\7020154002.txt

Output Set: N:\CRF4\04172003\I582340C.raw

62	115	120	125	
64	cag gtg aac ctg ctg cgg agg atg tgg gta aca ggt gtg gtg acg cag	492		
65	Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln			
66	130	135	140	
68	ggt gcc agc cgc ttg gcc agt cat gag tac ctg aag gcc ttc aag gtg	540		
69	Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val			
70	145	150	155	160
72	gcc tac agc ctt aat gga cac gaa ttc gat ttc atc cat gat gtt aat	588		
73	Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn			
74	165	170	175	
76	aaa aaa cac aag gag ttt gtg ggt aac tgg aac aaa aac gcg gtg cat	636		
77	Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His			
78	180	185	190	
80	gtc aac ctg ttt gag acc cct gtg gag gct cag tac gtg aga ttg tac	684		
81	Val Asn Leu Phe Glu Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr			
82	195	200	205	
84	ccc acg agc tgc cac acg gcc tgc act ctg cgc ttt gag cta ctg ggc	732		
85	Pro Thr Ser Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly			
86	210	215	220	
88	tgt gag ctg aac gga tgc gcc aat ccc ctg ggc ctg aag aat aac agc	780		
89	Cys Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser			
90	225	230	235	240
92	atc cct gac aag cag atc acg gcc tcc agc agc tac aag acc tgg ggc	828		
93	Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly			
94	245	250	255	
96	ttg cat ctc ttc agc tgg aac ccc tcc tat gca cgg ctg gac aag cag	876		
97	Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg Leu Asp Lys Gln			
98	260	265	270	
100	ggc aac ttc aac gcc tgg gtt gcg ggg agc tac ggt aac gat cag tgg	924		
101	Gly Asn Phe Asn Ala Trp Val Ala Gly Ser Tyr Gly Asn Asp Gln Trp			
102	275	280	285	
104	ctg cag gtg gac ctg ggc tcc tcg aag gag gtg aca ggc atc atc acc	972		
105	Leu Gln Val Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr			
106	290	295	300	
108	cag ggg gcc cgt aac ttt ggc tct gtc cag ttt gtg gca tcc tac aag	1020		
109	Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys			
110	305	310	315	320
112	gtt gcc tac agt aat gac agt gcg aac tgg act gag tac cag gac ccc	1068		
113	Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro			
114	325	330	335	
116	agg act ggc agc agt aag atc ttc cct ggc aac tgg gac aac cac tcc	1116		
117	Arg Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser			
118	340	345	350	
120	cac aag aag aac ttg ttt gag acg ccc atc ctg gct cgc tat gtg cgc	1164		
121	His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg			
122	355	360	365	
124	atc ctg cct gta gcc tgg cac aac cgc atc gcc ctg cgc ctg gag ctg	1212		
125	Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu Arg Leu Glu Leu			
126	370	375	380	

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```

128 ctg ggc tgt tag tggccacctg ccacccccag gtcttctctgc tttccatggg      1264
129 Leu Gly Cys
130 385
132 cccgctgcct cttggcttct cagccccctt aaatcaccat agggctgggg actggggaag      1324
134 gggagggtgt tcagaggcag caccaccaca cagtcacccc tccctccctc tttcccaccc      1384
136 tccacctctc acggggccctg ccccagcccc taagccccgt cccctaacc ccagtcctca      1444
138 ctgtcctgtt ttcttaggca ctgagggatc tgagtaggtc tgggatggac aggaaagggc      1504
140 aaagtagggc gtgtggtttc cctgccccctg tccggaccgc cgatcccagg tgcgtgtgtc      1564
142 tctgtctctc ctagccccctc tctcacacat cacattccca tggtaggcctc aagaaaggcc      1624
144 cggaagcccc aggctggaga taacagcctc ttgccgctcg gccctgcgtc ggcctgggg      1684
146 taccatgtgc cacaactgct gtggccccct gtccccaaga cacttcccct tgtctccctg      1744
148 gttgcctctc ttgcccttg tctgaagcc cagcgacaca gaaggggggtg gggcggtgtct      1804
150 atggggagaa agggagcgag gtcagaggag ccggcatggg ttggcagggt gggcggtttg      1864
152 ggccctcatg ctggcttttc accccagagg acacaggcag cttccaaaat atatttatct      1924
154 ttttcacggg      1934
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 387
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 2
164 Met Pro Arg Pro Arg Leu Leu Ala Ala Leu Cys Gly Ala Leu Leu Cys
165 1 5 10 15
168 Ala Pro Ser Leu Leu Val Ala Leu Asp Ile Cys Ser Lys Asn Pro Cys
169 20 25 30
172 His Asn Gly Gly Leu Cys Glu Glu Ile Ser Gln Glu Val Arg Gly Asp
173 35 40 45
176 Val Phe Pro Ser Tyr Thr Cys Thr Cys Leu Lys Gly Tyr Ala Gly Asn
177 50 55 60
180 His Cys Glu Thr Lys Cys Val Glu Pro Leu Gly Met Glu Asn Gly Asn
181 65 70 75 80
184 Ile Ala Asn Ser Gln Ile Ala Ala Ser Ser Val Arg Val Thr Phe Leu
185 85 90 95
188 Gly Leu Gln His Trp Val Pro Glu Leu Ala Arg Leu Asn Arg Ala Gly
189 100 105 110
192 Met Val Asn Ala Trp Thr Pro Ser Ser Asn Asp Asp Asn Pro Trp Ile
193 115 120 125
196 Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln
197 130 135 140
200 Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val
201 145 150 155 160
204 Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn
205 165 170 175
208 Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His
209 180 185 190
212 Val Asn Leu Phe Glu Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr
213 195 200 205
216 Pro Thr Ser Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly
217 210 215 220
220 Cys Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser

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```

221 225          230          235          240
224 Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly
225          245          250          255
228 Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg Leu Asp Lys Gln
229          260          265          270
232 Gly Asn Phe Asn Ala Trp Val Ala Gly Ser Tyr Gly Asn Asp Gln Trp
233          275          280          285
236 Leu Gln Val Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr
237          290          295          300
240 Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys
241 305          310          315          320
244 Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro
245          325          330          335
248 Arg Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
249          340          345          350
252 His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg
253          355          360          365
256 Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu Arg Leu Glu Leu
257          370          375          380
260 Leu Gly Cys

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261 385

264 <210> SEQ ID NO: 3

265 <211> LENGTH: 2077

266 <212> TYPE: DNA

267 <213> ORGANISM: Murine

269 <220> FEATURE:

270 <221> NAME/KEY: CDS

271 <222> LOCATION: (46)..(1434)

272 <223> OTHER INFORMATION:

W--> 274 <400> 3

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275 gaattccgca tcagagcgcg tggacctttt cccgcgtccc gcagc atg cag gtc tcc      57
276                                     Met Gln Val Ser
277                                     1
279 cgt gtg ctg gcc gcg ctg tgc ggc atg cta ctc tgc gcc tct ggc ctc      105
280 Arg Val Leu Ala Ala Leu Cys Gly Met Leu Leu Cys Ala Ser Gly Leu
281 5          10          15          20
283 ttc gcc gcg tct ggt gac ttc tgt gac tcc agc ctg tgc ctg aac ggt      153
284 Phe Ala Ala Ser Gly Asp Phe Cys Asp Ser Ser Leu Cys Leu Asn Gly
285          25          30          35
287 ggc acc tgc ttg acg ggc caa gac aat gac atc tac tgc ctc tgc cct      201
288 Gly Thr Cys Leu Thr Gly Gln Asp Asn Asp Ile Tyr Cys Leu Cys Pro
289          40          45          50
291 gaa ggc ttc aca ggc ctt gtg tgc aat gag act gag aga gga cca tgc      249
292 Glu Gly Phe Thr Gly Leu Val Cys Asn Glu Thr Glu Arg Gly Pro Cys
293          55          60          65
295 tcc cca aac cct tgc tac aat gat gcc aaa tgt ctg gtg act ttg gac      297
296 Ser Pro Asn Pro Cys Tyr Asn Asp Ala Lys Cys Leu Val Thr Leu Asp
297          70          75          80
299 aca cag cgt ggg gac atc ttc acc gaa tac atc tgc cag tgc cct gtg      345

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300	Thr	Gln	Arg	Gly	Asp	Ile	Phe	Thr	Glu	Tyr	Ile	Cys	Gln	Cys	Pro	Val	
301	85					90					95					100	
303	ggc	tac	tcg	ggc	atc	cac	tgt	gaa	acc	gag	acc	aac	tac	tac	aac	ctg	393
304	Gly	Tyr	Ser	Gly	Ile	His	Cys	Glu	Thr	Glu	Thr	Asn	Tyr	Tyr	Asn	Leu	
305					105					110					115		
307	gat	gga	gaa	tac	atg	ttc	acc	aca	gcc	gtc	ccc	aat	act	gcc	gtc	ccc	441
308	Asp	Gly	Glu	Tyr	Met	Phe	Thr	Thr	Ala	Val	Pro	Asn	Thr	Ala	Val	Pro	
309				120					125					130			
311	acc	ccg	gcc	ccc	acc	ccc	gat	ctt	tcc	aac	aac	cta	gcc	tcc	cgt	tgt	489
312	Thr	Pro	Ala	Pro	Thr	Pro	Asp	Leu	Ser	Asn	Asn	Leu	Ala	Ser	Arg	Cys	
313				135					140					145			
315	tct	aca	cag	ctg	ggc	atg	gaa	ggg	ggc	gcc	att	gct	gat	tca	cag	att	537
316	Ser	Thr	Gln	Leu	Gly	Met	Glu	Gly	Gly	Ala	Ile	Ala	Asp	Ser	Gln	Ile	
317		150				155					160						
319	tcc	gcc	tcg	tat	gtg	tat	atg	ggt	ttc	atg	ggc	ttg	cag	cgc	tgg	ggc	585
320	Ser	Ala	Ser	Tyr	Val	Tyr	Met	Gly	Phe	Met	Gly	Leu	Gln	Arg	Trp	Gly	
321	165				170					175					180		
323	ccg	gag	ctg	gct	cgt	ctg	tac	cgc	aca	ggg	atc	gtc	aat	gcc	tgg	cac	633
324	Pro	Glu	Leu	Ala	Arg	Leu	Tyr	Arg	Thr	Gly	Ile	Val	Asn	Ala	Trp	His	
325				185					190						195		
327	gcc	agc	aac	tat	gat	agc	aag	ccc	tgg	atc	cag	gtg	aac	ctt	ctg	cgg	681
328	Ala	Ser	Asn	Tyr	Asp	Ser	Lys	Pro	Trp	Ile	Gln	Val	Asn	Leu	Leu	Arg	
329				200					205					210			
331	aag	atg	cgg	gta	tca	ggt	gtg	atg	acg	cag	ggt	gcc	agc	cgt	gcc	ggg	729
332	Lys	Met	Arg	Val	Ser	Gly	Val	Met	Thr	Gln	Gly	Ala	Ser	Arg	Ala	Gly	
333			215				220						225				
335	agg	gcg	gag	tac	ctg	aag	acc	ttc	aag	gtg	gct	tac	agc	ctc	gac	gga	777
336	Arg	Ala	Glu	Tyr	Leu	Lys	Thr	Phe	Lys	Val	Ala	Tyr	Ser	Leu	Asp	Gly	
337		230				235					240						
339	cgc	aag	ttt	gag	ttc	atc	cag	gat	gaa	agc	ggt	gga	gac	aag	gag	ttt	825
340	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp	Lys	Glu	Phe	
341	245				250					255					260		
343	ttg	ggt	aac	ctg	gac	aac	aac	agc	ctg	aag	gtt	aac	atg	ttc	aac	ccg	873
344	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met	Phe	Asn	Pro	
345				265					270					275			
347	act	ctg	gag	gca	cag	tac	ata	agg	ctg	tac	cct	gtt	tcg	tgc	cac	cgc	921
348	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser	Cys	His	Arg	
349				280					285					290			
351	ggc	tgc	acc	ctc	cgc	ttc	gag	ctc	ctg	ggc	tgt	gag	ttg	cac	gga	tgt	969
352	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu	His	Gly	Cys	
353			295				300					305					
355	ctc	gag	ccc	ctg	ggc	ctg	aag	aat	aac	aca	att	cct	gac	agc	cag	atg	1017
356	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp	Ser	Gln	Met	
357		310				315					320						
359	tca	gcc	tcc	agc	agc	tac	aag	aca	tgg	aac	ctg	cgt	gct	ttt	ggc	tgg	1065
360	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala	Phe	Gly	Trp	
361	325				330					335					340		
363	tac	ccc	cac	ttg	gga	agg	ctg	gat	aat	cag	ggc	aag	atc	aat	gcc	tgg	1113
364	Tyr	Pro	His	Leu	Gly	Arg	Leu	Asp	Asn	Gln	Gly	Lys	Ile	Asn	Ala	Trp	

VERIFICATION SUMMARY

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L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27

L:274 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:272